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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,732

DATE: 01/23/2002

TIME: 14:42:21

Input Set : N:\Crif3\RULE60\09905732.raw

Output Set: N:\CRF3\01232002\I905732.raw

1 <110> APPLICANT: Chadwick, Brian Paul
2 Frischauf, Anna-Maria
3 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
4 POLYPEPTIDES AND NUCLEIC ACIDS
5 <130> FILE REFERENCE: 9598-066
6 <140> CURRENT APPLICATION NUMBER: 09/905,732
7 <141> CURRENT FILING DATE: 2001-07-13
9 <150> PRIOR APPLICATION NUMBER: US/09/240,639
10 <151> PRIOR FILING DATE: 1998-01-29
13 <160> NUMBER OF SEQ ID NOS: 29
14 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2762
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (232)..(1599)
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26 gcgcggtgca tggaatggc tatgtgaatg aaaaaaggta tccgttatga aacttccaga 180
27 aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga 237
28 Met Arg
29 1
30 aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
31 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
32 5 10 15
33 ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
34 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
35 20 25 30
36 cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
37 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
38 35 40 45 50
39 ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
40 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
41 55 60 65
42 gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
43 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
44 70 75 80
45 act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525
46 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
47 85 90 95

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48	act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt	573
49	Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
50	100 105 110	
51	tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa	621
52	Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
53	115 120 125 130	
54	cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc	669
55	Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
56	135 140 145	
57	acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga	717
58	Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
59	150 155 160	
60	gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca	765
61	Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
62	165 170 175	
63	tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca	813
64	Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
65	180 185 190	
66	gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc	861
67	Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
68	195 200 205 210	
69	ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga	909
70	Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
71	215 220 225	
72	gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag	957
73	Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln	
74	230 235 240	
75	gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc	1005
76	Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr	
77	245 250 255	
78	tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca	1053
79	Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala	
80	260 265 270	
81	cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga	1101
82	Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly	
83	275 280 285 290	
84	aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg	1149
85	Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp	
86	295 300 305	
87	gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca	1197
88	Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala	
89	310 315 320	
90	agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac	1245
91	Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn	
92	325 330 335	
93	aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc	1293
94	Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe	
95	340 345 350	
96	tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag	1341

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97 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
98 355 360 365 370
99 aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac 1389
100 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
101 375 380 385
102 gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc 1437
103 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
104 390 395 400
105 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc 1485
106 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
107 405 410 415
108 agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc 1533
109 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
110 420 425 430
111 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga 1581
112 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
113 435 440 445 450
114 cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag 1629
115 Gln Lys Ser Pro Ala Ser
116 455
117 cagtgtctgt gtgtctgcat aaaccctcct gtccctggacg tgacttcacg ctgaggagcc 1689
118 acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg 1749
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121 aggcacacac tgagggggca gtgtggtctc ctgcctgtcc catcccatg ccccgctccg 1929
122 ggggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca 1989
123 gtttctctcc cagggcagag ctcctcttcc tgcaagagtc tgggaggcgg tgcaggctgt 2049
124 cctggctgct ctggggaagc cgagggaacg ccataacacc cccgggacag taggtctggg 2109
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132 cgggccacca tccgccacc tggggtgac cccacctctt ccatggacag tgtgagcccc 2589
133 gggccgtgca tctgtctcag tgtggcgtca gtgtcggggc tgagccctt gagctgttc 2649
134 agtgaatgta cagtgcctcg cagagctga acctcatgtg ttccactccc aataaaaggt 2709
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143 1 5 10 15
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145 20 25 30
146 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
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150	Thr	Ala	Ala	Asp	Gly	His	Glu	Val	Phe	Tyr	Gly	Ile	Met	Phe	Asp	Ala	
151			65				70					75					80
152	Gly	Ser	Thr	Gly	Thr	Arg	Val	His	Val	Phe	Gln	Phe	Thr	Arg	Pro	Pro	
153						85					90				95		
154	Arg	Glu	Thr	Pro	Thr	Leu	Thr	His	Glu	Thr	Phe	Lys	Ala	Val	Lys	Pro	
155				100					105					110			
156	Gly	Leu	Ser	Ala	Tyr	Ala	Asp	Asp	Val	Glu	Lys	Ser	Ala	Gln	Gly	Ile	
157				115				120					125				
158	Arg	Glu	Leu	Leu	Asp	Val	Ala	Lys	Gln	Asp	Ile	Pro	Phe	Asp	Phe	Trp	
159				130				135					140				
160	Lys	Ala	Thr	Pro	Leu	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	
161						150						155				160	
162	Pro	Gly	Glu	Lys	Ala	Gln	Lys	Leu	Leu	Gln	Lys	Val	Lys	Glu	Val	Phe	
163					165					170					175		
164	Lys	Ala	Ser	Pro	Phe	Leu	Val	Gly	Asp	Asp	Cys	Val	Ser	Ile	Met	Asn	
165				180					185					190			
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169				210			215					220					
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173					245					250					255		
174	Arg	Thr	Tyr	Lys	Leu	Tyr	Ser	Tyr	Ser	Tyr	Leu	Gly	Leu	Gly	Leu	Met	
175				260					265					270			
176	Ser	Ala	Arg	Leu	Ala	Ile	Leu	Gly	Gly	Val	Glu	Gly	Gln	Pro	Ala	Lys	
177				275				280					285				
178	Asp	Gly	Lys	Glu	Leu	Val	Ser	Pro	Cys	Leu	Ser	Pro	Ser	Phe	Lys	Gly	
179				290			295					300					
180	Glu	Trp	Glu	His	Ala	Glu	Val	Thr	Tyr	Arg	Val	Ser	Gly	Gln	Lys	Ala	
181						310					315					320	
182	Ala	Ala	Ser	Leu	His	Glu	Leu	Cys	Ala	Ala	Arg	Val	Ser	Glu	Val	Leu	
183					325					330					335		
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185				340					345					350			
186	Ala</																

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211                      Met Phe Thr Val Leu Thr Arg Gln Pro Cys
212                      1                      5                      10
213      gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc 160
214      Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
215                      15                      20                      25
216      ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc 208
217      Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
218                      30                      35                      40
219      atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt 256
220      Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
221                      45                      50                      55
222      att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa 304
223      Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
224                      60                      65                      70
225      tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc 352
226      Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
227      75                      80                      85                      90
228      aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc 400
229      Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
230                      95                      100                      105
231      caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg 448
232      Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
233                      110                      115                      120
234      cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc 496
235      Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
236                      125                      130                      135
237      acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat 544
238      Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
239                      140                      145                      150
240      gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac 592
241      Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
242      155                      160                      165                      170
243      ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga 640
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